



FIGURE 1

SEQ ID NO: 1

>STAAU_R009 nucleotide sequence: 1800

TTGCGAATAGATCAATCGATCATTAATGAAATAAAAGATAAAACCGACATTTTAGACTTGGTAAAGTGA
ATATGTAAAATTAGAAAAGAGAGGACGCAATTATATAGGTTTGTGTCCTTTTCATGATGAAAAGACAC
CTTCATTTACAGTTTCTGAAGATAAAACAAATTTGTCAATTGTTTTGGTTGTAAAAAAGGTGGCAATGTT
TTTCAATTTACTCAAGAAATTAAAGACATATCATTGTTGAAGCGGTTAAAGAATTAGGTGATAGAGT
TAATGTTGCTGTAGATATTGAGGCAACACAATCTAACTCAAATGTTCAAATTGCTTCTGATGATTTAC
AAATGATTGAAATGCATGAGTTAATACAAGAATTTTATTATTACGCTTTAACAAAGACAGTCGAAGGC
GAACAAGCATTAAACGTACTTACAAGAACGTGGTTTTACAGATGCGCTTATTAAAGAGCGAGGCATTGG
CTTTGCACCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAAAGGGTTACGATATTGAATTAG
CATATGAAGCCGGATTATTATCACGTAACGAAGAAAATTTTCAAGTTATTACGATAGATTTTCAAAATCGT
ATTATGTTTCTTTGAAAAATGCGCAAGGAAGAATTGTTGGATATTCAAGTCGAACATATAACCGGTCA
AGAACCAAAATACTTAAATAGTCCTGAAACACCTATCTTTCAAAAAAGAAAGTTGTTATACAACCTTAG
ATAAAGCGCGTAAATCAATTAGAAAATTAGATGAAATCGTATTACTAGAAGGTTTTATGGATGTTATA
AAATCTGATACTGCTGGCTTGAAAAACGTTGTTGCAACAATGGGTACACAGTTGTCAGATGAACATAT
TACTTTTATACGAAAGTTAAACATCAAATATAACATTAATGTTTGATGGGGATTTTGCAGGTTAGTGAAG
CAACACTTAAACAGGTCAAAATTTGTTACAGCAAGGGCTAAATGTATTTGTTATACAATTGCCATCA
GGCATGGATCCGGATGAATACATTGGTAAGTATGGCAACGATGCATTTACTGCTTTTGTAAAAAATGA
CAAAAAGTCATTTGCACATTATAAAGTGAGTATATTAAGAATGAAATTGCACATAATGACCTTTCAT
ATGAACGTTATTTGAAAGAACTAAGTCATGATATTTGCTTATGAAATCATCGATTTTGAACAAAAAG
GCTTTAAATGATGTTGCACCATTTTCAATGTTAGTCCTGAGCAATTAGCTAACGAAATACAATTCAA
TCAAGCACCAGCCAATTATTATCCAGAAGATGAGTATGGCGGTTACATTGAACCTGAGCCAATTGGTA
TGGCACAATTTGACAATTTGAGCCGTCAAGAAAAAGCGGAGCGAGCATTTTAAAAACATTTAATGAGA
GATAAAGATACATTTTAAATTATTATGAAAGTGTGATAAGGATAACTTCACAAATCAGCATTTTAA
ATATGTATTCGAAGTCTTACATGATTTTTATGCGGAAAATGATCAATATAATATCAGTGATGCTGTGC
AGTATGTTAATTCAAATGAGTTGAGAGAAACACTAATTAGCTTAGAACAATATAATTTGAATGACGAA
CCATATGAAAATGAAATTGATGATTATGTCAATGTTATTAATGAAAAAGGACAAGAAACAATTGAGTC
ATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTAGAATTACAAAAATACTATTTACAGC
AAATTGTTGCTAAGAATAAAGAACGCATGTAG

SEQ ID NO: 2

>STAAU_R009 amino acid sequence : 599

LRIDQSIINEIKDKTDILDVSEYVKLEKRGRNYIGLCPFHDEKTPSFTVSEDKQICHCFGCKKGGNV
FQFTQEIKDIFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQMIEMHELIQEFYYYYALTKTVEG
EQALTYLQERGFDDALIKERGIGFAPDSSHFCHDFLQKKGYDIELAYEAGLLSRNEENFSYYDRFRNR
IMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEGFMDVI
KSDTAGLKNVATMGTQLSDEHITFIRKLTSNITLMFDGDFAGSEATLKTGQNLQQLNVFVIQLPS
GMDPDEYIGKYGNDAFVAVKNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQOK
ALNDVAPFFNVSPPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAEAFKHLMR
DKDTFLNYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLISLEQYNLNDE
PYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQKYLLQIVAKNKERM



FIGURE 3C.

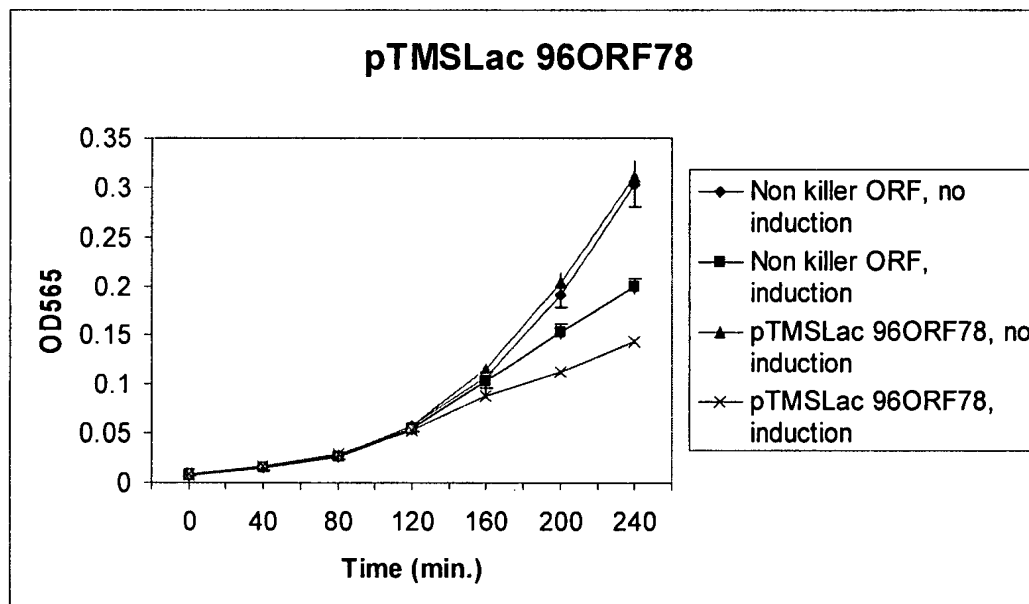
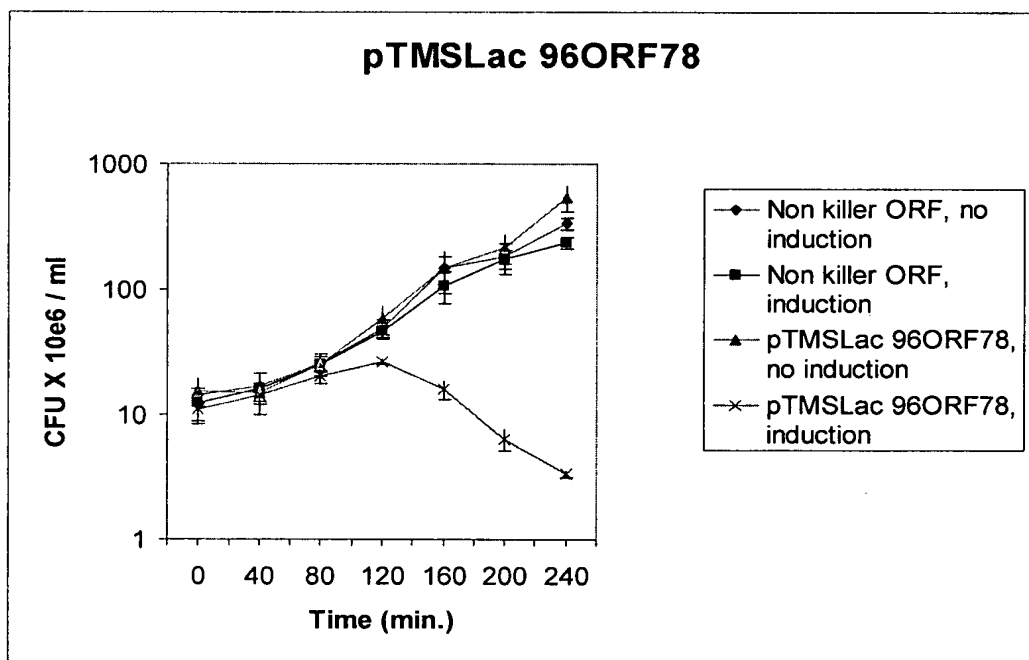


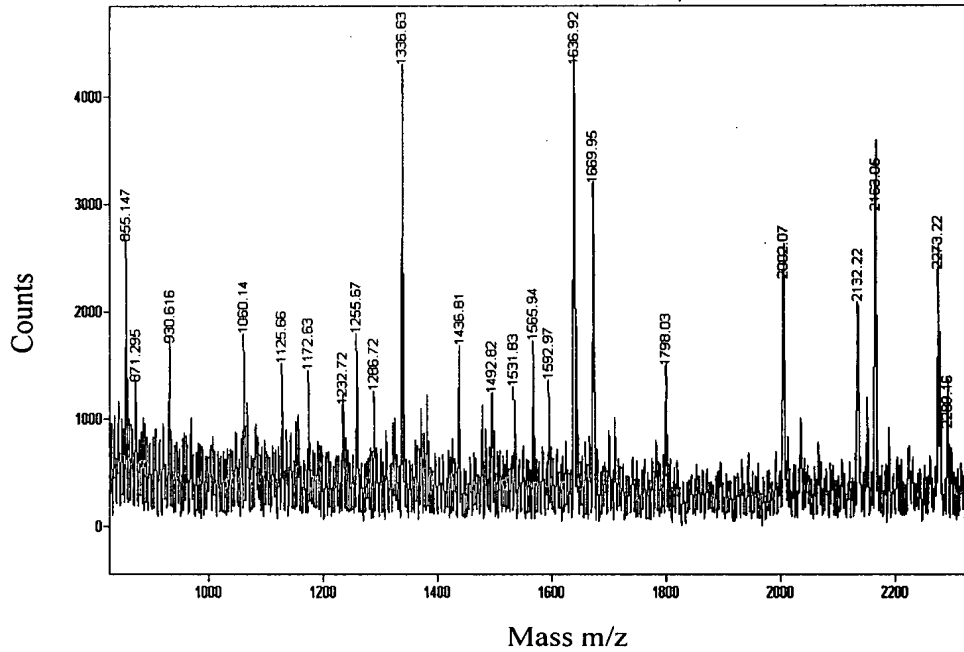
FIGURE 3D.





Replacement Sheet

FIGURE 6



Details for rank 1 candidate in search 20000915095311-0166-127000000001

ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID : orf78 72 [Pass:0]

Measured peptides : 23

Matched peptides : 7

Min. sequence coverage: 14%



Measured Avg/ Computed Error Residues Missed

Mass(M) Mono Mass (Da) Start To Cut Peptide sequence

1124.649	M	1124.622	0.027	588	596	0	YYLQQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDISLMK
1171.623	M	1171.644	-0.021	5	14	0	IDQSIINEIK
1254.661	M	1254.620	0.041	563	573	0	GQETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENFSYYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYR

Unmatched Monoisotopic Masses:

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.943 1592.967
1636.921 1669.948 2132.217 2163.048 2273.222 2289.164



FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:

domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55

```
*->ipeesIdeLknriDIVdvisYVklKkGrnYkgLCPFHdEKTSPFS
i++++I+e+k+++DI d++seYVkl+K+GrnY+gLCPFHdEKTSPF+
gi|133988      3   IDQSIINEIKDKTDILDVSEYVKLEKRGRNYIGLCPFHdEKTSPFT 49

VspeKqfYhCFGCGagGdaIkFlmkyeklsFvEAvekLAdragidlpYek
Vs +Kq+ hCFGc++gG+++ F +++++sFVEAV++L dr+++ +++e
gi|133988      50 VSEDKQICHCFGCKKGGNVFQFTQEIKDISFVEAVKELGDRVNVAVDIEA 99

g<-*
+
gi|133988      100 T      100
```

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

```
*->kvliiVEgpsdakalalalgkpskrkivYelpggkdgnvvaslGhlv
+++++ Eg++d+++ a+ +nvva++G+
gi|133988      260 DEIVLLEGFMDVIKSDTAGL-----KNVVATMGQTQ- 289

dLptpegyddkykwlwlpivdvkkgfepyqiefdqlckcskkidlkkeql
l++e++
gi|133988      290 -----LSDEHI 295

kllkklakkadevilatDpDreGeaiawkllellkpygpveleddkkvr
++kl+++ + l++D+D +G ++++k + l+ +g +v++
gi|133988      296 TFIRKLTSN---ITLMFDGDFAGSEATLKTGQNLLQQGL-----NVFV 335

iflp<-*
i+lp
gi|133988      336 IQLP      339
```



FIGURE 7B/1

B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM_STAAU DNA PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)
 Sequence 2 STAAU_R009 STAAU_R009_NT|1-1800|(599 letters)

Identical: 560/605 (92%), Similar: 564/605 (93%), Gap: 39/605 (6%)

seq1	1 M-----	-----IGLCPFHDEKTPSFTVSEDKQICHCF	27
	:		
seq2	1 LRIDQSIINEIKDKTDILDVLVSEYVLEKGRNRYIGLCPFHDEKTPSFTVSEDKQICHCF		60
seq1	28 GCKKGNVFQFTQEIKDISFVEAVKELGDRVNVAVDIEATQNSNVQIASDDDLQMIEMHE		87
seq2	61 GCKKGNVFQFTQEIKDISFVEAVKELGDRVNVAVDIEATQNSNVQIASDDDLQMIEMHE		120
seq1	88 LIQEFYYVALTKTVEGEQALTYLQERGFTDALIKERGIGFAPDSSHFCDFLOKKGYDIE		147
seq2	121 LIQEFYYVALTKTVEGEQALTYLQERGFTDALIKERGIGFAPDSSHFCDFLOKKGYDIE		180
seq1	148 LAYEAGLLSRNEENFSYDRFRNRIMFPLKNAQGRIVGSGRTYTGQEPKYLNSPETPIF		207
seq2	181 LAYEAGLLSRNEENFSYDRFRNRIMFPLKNAQGRIVGSGRTYTGQEPKYLNSPETPIF		240
seq1	208 QKRKLLYNLDKARKSIRKLDIEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEITFIRK		267
seq2	241 QKRKLLYNLDKARKSIRKLDIEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEITFIRK		300
seq1	268 LTSNITLMFDGDFAGSEATLKTGQHLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTTFV		327
seq2	301 LTSNITLMFDGDFAGSEATLKTGQNLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFV		360
seq1	328 KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQOKAINDVAPFFNV		387
seq2	361 KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQOKALNDVAPFFNV		420
seq1	388 PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFCLKHL		447
seq2	421 PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKAEERAFCLKHL		474

seq1		448	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLLI	507
seq2		475	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLLI	534
seq1		508	SLEQYNLNGEPYENEIDDDYVNVINKEKGQTIESLNHKLREATRIGDVELQKYVLQQIVAK	567
seq2		535	SLEQYNLNDPEYENEIDDDYVNVINKEKGQTIESLNHKLREATRIGDVELQKYVLQQIVAK	594
seq1		568	NKERM 572	
seq2		595	NKERM 599	

seq1	1	L-RIDQSIINEIKDKTDILDLVSEYVKLEKGRNVIGLCPFHDEKTPSFTVSEDKQICH	58
seq2	1	MGRIPPEETIEAIRRGVDIVDIGEYVQLKRQGRNVFGLCPFHEGKTPSFVSPEKQIFH	60
seq1	59	CFGCKKGNVFQTFQEIKDIFSVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQ-MIE	117
seq2	61	CFGCGAGGNAFTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELDVGRDDGQTDEAKAMTE	120
seq1	118	MHELIQEFYYVALTKTVEGEQALTYLQERGFDTALIKERGIGFAPDSSHCHDFLOKKGY	177
seq2	121	AHALLKRFYHLLLVHTKEGQALDYLQARGWTKETIDRFEIGYAPDAPDAAAKLLESHSF	180
seq1	178	DIELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLSNPET	237
seq2	181	SLPVMEKAGLLTKKEDG-RVYGRFRNRIMFPIHDHRETGVFGSRLGLEGHPKYVNSNPET	239

Replacement Sheet

FIGURE 7B/3

seq1	238	PIFQKRKLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLKNVVATMGTSLSDEHITF	297
seq2	240	PVFRKGAILYHFAARVPIRKQRQALLVEGFADVISAAQAGIDYAIATMGTSLTEEQARI	299
seq1	298	IRKLTSNITLMTDFDGFAGSEATLKTGQNLQQLNVFVIQLPSGMDPDEYIGKYGNDAFT	357
seq2	300	LRP-CDTITICYDGDRAIEAAWAAAEQLSALGCRVKVASLPNGLDPDEYIRVYGGERF-	357
seq1	358	AFVKNKKSFHYKVSILKDEIAHNDLSYE---RYLKELSHDISLMKSSILQQKALNDV	413
seq2	358	AGEAGCRRPLVAFKWAYLR--RGKNLQHEGERLRYIDEALREIGKLSPPVEQDYVLRQL	414
seq1	414	APFFNVSPQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAEAFKX	473
seq2	415	AEFSLSLSALHEQLSRQERTKPREAPDGETARP---MLAKKLLPAFQNAERLLLAH	470
seq1	474	LMRDKDTFLNYYESVDKDNFTNQHFXYVFEVLHDFYAENDQYNISDAVQYVNSNELRETL	533
seq2	471	MMRSRDVALVVQERIG-GRFNIEHRALAAIYAFYEEGHEADPGALISRI-PGELQPLA	528
seq1	534	ISLEQYNLNDEPYENEIDYV-NVINEKGOETIESLNHKLREATRIGDVELQKYVLOQIV	592
seq2	529	SDVSLLLTADDVSEQELEDYIRHVLNRPKWLMLKVKEQKTEAERRKDFLTAARIAKEMI	588
seq1	593	AKNK--ERM	599
seq2	589	EMKKMLSSS	597



A circular black and white stamp. The outer ring contains the text "OIP" at the top and "PATENT & TRADEMARK OFFICE" at the bottom. In the center, the date "AUG 01 2007" is stamped.

Sequence 1 STAAU R009 599 letters)

Sequence 2 gi|130904|sp|P05096|PRIM BACSU DNA PRIMASE(603 letters)

Identical: 221/610 (36%), **Similar:** 334/610 (54%), **Gap:** 18/610 (2%)

[illegible]

seq1 59 CFGCKKGGNVFOFTOEIKDISFVEAVKELGDRVNVAVDIEATOSNSNVOIASDDLMIEM 118

seq2 61 CFGCGAGGNVFSFLROMEGYSFAESVSHLADKYOIDFPDDITVHSGARPESSGEOKMAEA 120

seq1 119 HELIOEFFYVYALTKTVEGEOALTYLOERGF^TDALIKERGIGFAPDSSHFCHDFLOKKG^{YD} 178

seq2 121 HELKKFYHLLINTKEGOEALDYLLSRGFTKELINEFOIGYALDSWDFITKFLVKRGFS 180

seq1 179 IELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAOGRIVGYSGRITYTGOEPKYLNSPETP 238

seq2 181 EAOMEKAGLLIRREDGSGYFDRFRNRVMFPIHDHGA VAFSGRALGSOOPKYMNSPETP 240

seq1 239 IFOKRLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLKNVVATMGTOLSDEHITFI 298

seq2 241 LFHKSKLLYNFYKARLHIRKOEAVLFEGFADVYTAVSSDVKESIATMGTSLTDDHVKIL 300

seq1 299 RKLTSNITLMFDGDFAGSEATLKTGONLLOOGLNVFVIOLPSGMDPDEYICKYGND AFTA 358

seq2 301 RRNVEEII LCYDSDKAGYEATLKASELLOKKGCKVRVAMIPDGLDPPDYIKKFGGEKEFN 360

seq1 359 FVKNDDKKSFAHYKVSIL-KDEIAHNDLSYERYLKELSHDISLMKSSSILOOKALNDVAPFF 417

seq2 361 DIIPASVTVMAFKMOYERKGNLSDEGDRIAYIKDVLKETSTLSGSLFOEVVVKOLASEF 420

```

seq1      418  NVSPEOLANEIOFNOAPANYYPEDGYIEPEPIGMAOFDNL SRO-----EKAERAF 470

```

seq2 421 SLSOESLTE--OLSVFSKONKPADNSG---ETKTRRAHLTTKAROKRLRPAYENAERLL 474

FIGURE 7B/5

seq1	471	LKHLMRDKDTFLNYYESVDKDNFTNQHFYFVEVLHDFYENDQYNISDAVQYVNSNELR	530
		: : : : : : : : : : : : : : :	
seq2	475	LAHMLRDRSVIKKVIDRVGFQFNIDEH-RALAAVLYAFYEEGAELTPQHLMARVTDHHS	533
		: : : : : : : : : : : : : : :	
seq1	531	ETLISLEQYNLNDPEYNEIDDV-VNINEKGOETIESLNHKLREATRIGDVELQKYYLQ	589
		: : : : : : : : : : : : : : :	
seq2	534	QLLSDILMLQVNLSEALSVDYVKVLNQRNWSMIKEKEAERAEARQKDFLRAASLAQ	593
		: : : : : : : : : : : : : : :	
seq1	590	QIVAKNKERM	599
		: :	
seq2	594	EIVTLNRSLK	603

Sequence 1 STAAU R009 (599 letters)

Sequence 2 gi|130908|sp|P02923|PRIM_ECOLI DNA PRIMASE (581 letters)

Identical: 170/619 (27%), **Similar:** 294/619 (47%), **Gap:** 58/619 (9%)

[illegible]

Replacement Sheet

FIGURE 7B/6

seq1	296	TFIRKLTSTNITLMTDFDGFAGSEA---TLKTGQNLQQGLNVFVIQLPSGMDPDDEYIGKYG	352
seq2	295	QLLFRAFNVICCYDGRAGRDAAWRALETALPYMTDGRQLRFMLPDGEDPDTLVRKEG	354
seq1	353	NDAFTAFVKNDKKSFAHYKVSILKDEIAHNDLSVERYLKELSHDISLMKSSILQQKALND	412
seq2	355	KEAFEARMEQAMPLSAFLFNSLMPQV-----DLS-----TPDGRARLSTLALPLISQVPGET	406
seq1	413	VAPFFNVSPQLANEIQF--NQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAERAF	470
seq2	407	LRIYLR---QELGNKLGILDDSQLERLMPKAAESGVSRPVP-----QLKRTTMRIL	454
seq1	471	LKHLMRDKD--TFLNYVESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNE	528
seq2	455	IGLLVQNPELATLVPPLENLDENKLPGLG---LFRELVNTCLSQPGLTTGQLLEHYRGTN	511
seq1	529	LRETLISLEQY-----NLNDEPYENEIDDDYVNVINEKQOETIESLNHKLREATR--IGD	580
seq2	512	NAATLEKLSMWDDIADKNIAEQFTDSLNHMFDSLLELRQEEELIA-----RERTHGLSNE	566
seq1	581	VELQYYYLQOIIVAKNKERM	599
seq2	567	ERLELWTLNQELAKK-----	581

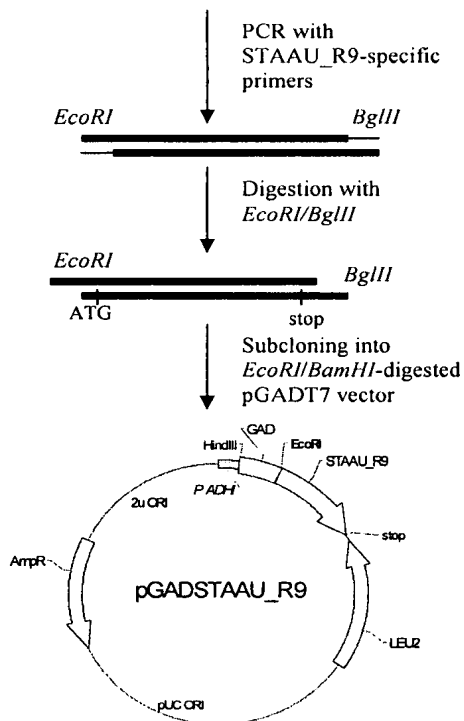




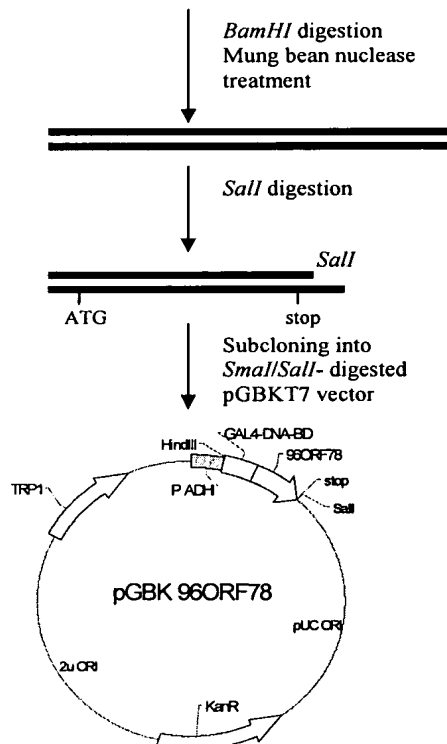
Replacement Sheet

FIGURE 8

A- *Staphylococcus aureus* genomic DNA



B- 96pTMSMLacORF78



C-

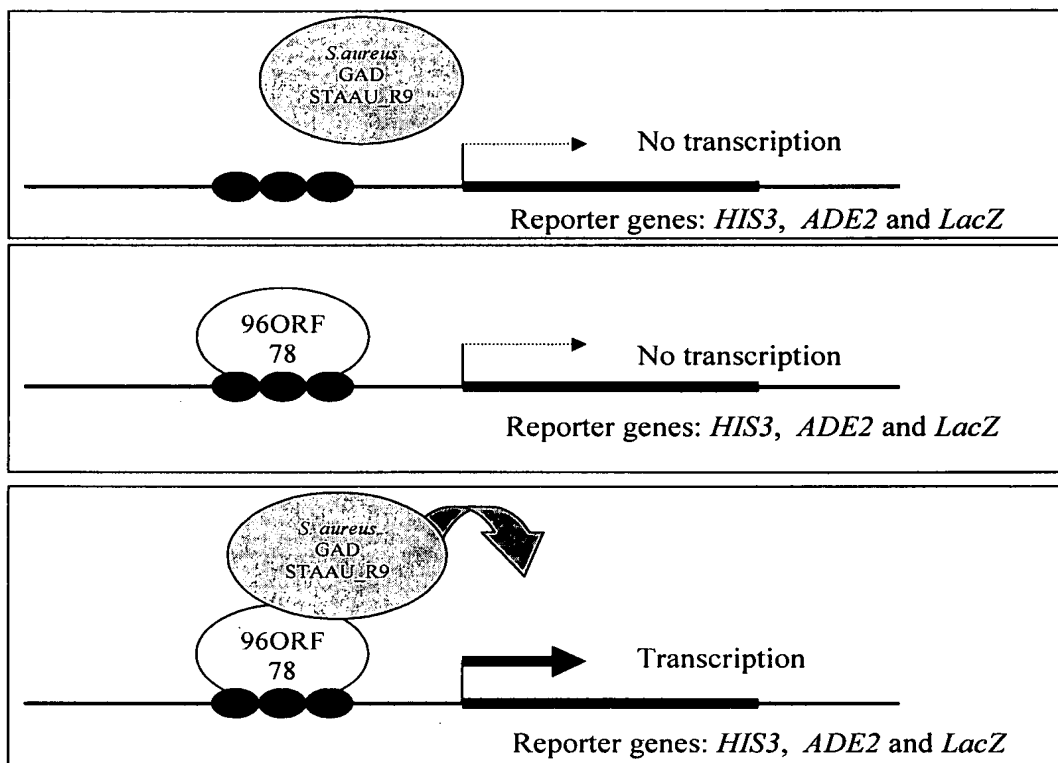
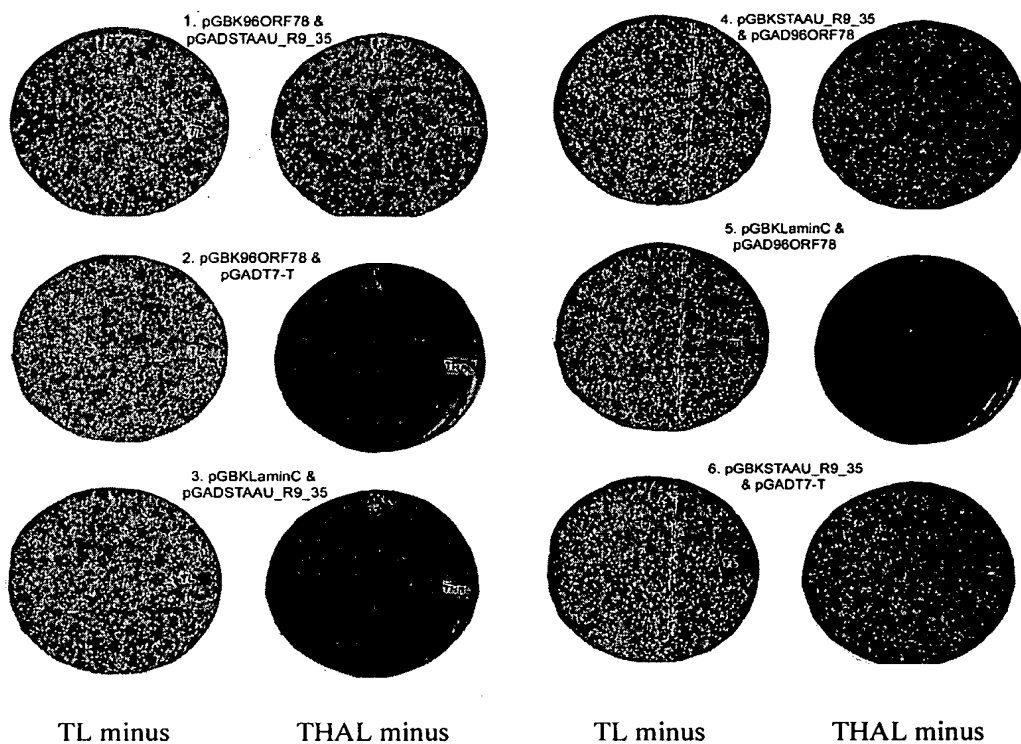


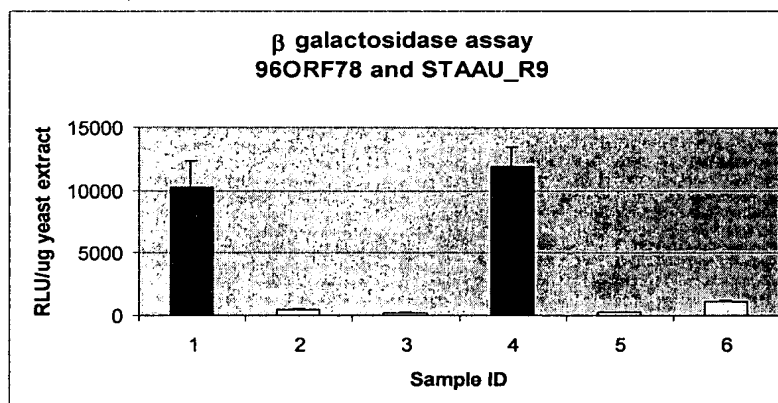


FIGURE 9

A.



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10, 250	2, 080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11, 935	1, 477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1, 121	37

FIGURE 10

Replacement Sheet

A. Fragments of STAAU_R9

B.

Interaction with
96ORF78

1	599	Yes
35	599	Yes
35	342	No
229	402	No
229	599	Yes
380	599	Yes
380	449	No
380	490	No
380	530	No
380	561	No
449	599	Yes
490	599	Yes
530	599	Yes
561	599	Yes

SEQ ID NO: 6 STAAU_R9_561-599
AMINO ACID SEQUENCE

GQETIESLNHKLREATRIGDVELQKYLLQQIVAKNKERM

SEQ ID NO: 5 STAAU_R9_1683-1800
NUCLEIC ACID SEQUENCE

GGACAAAGAAACAATTGAGTCATTGAATCATATAATTAGGGAAGCTACAAGGATTGGCGATGTA
GAATTACAAAATACTATTACAGCAAAATTGTTGCTAAGAATAAAGAACGCATGTAG

C.

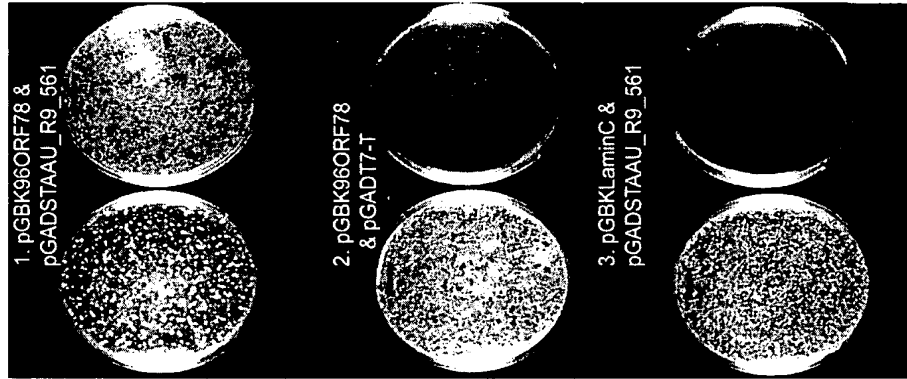




Figure 11 A.

	Primer name	Primer sequence	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatctCTACATGCGTTCTTTATTC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAAATACCTAAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcgatccATGCCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTCTATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcgatccctaAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcgatccctaCTTATCAACACTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcgatccctaTCTCAACTCATTGAATTAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcgatccctaTCCTTTTTCATTAATAACATTG-3'	BamHI

Figure 11 B.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG